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EXPRESSION SYSTEMS

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# Sequence and Method for Increasing Protein Expression in Cellular Expression Systems

## Background of the Invention

5 Proteins are needed for a variety of uses, especially for commercial food and chemical production and for medically therapeutic uses. These proteins may not be readily isolated from their natural sources, or may be needed in a mutated, or non-naturally occurring form. In such cases expression of heterologous proteins from cellular expression systems has proven useful.

10 Cellular expression systems rely on host cells, such as bacterial, yeast, fungal, and mammalian cells for expression of heterologous proteins. Bacterial cells provide an advantage in terms of ease of cultivation on inexpensive growth media and ease of manipulation of heterologous gene expression vectors. Heterologous proteins produced in bacterial expression systems can be isolated  
15 from inclusion bodies produced within the bacteria. They can also be isolated from the periplasmic space if the heterologous protein has been expressed in conjunction with a signal recognition sequence, or leader sequence, that directs the protein through the bacterial secretory pathway. Bacterial systems have been found to be disadvantageous, however, for expression of certain eukaryotic  
20 proteins, because they do not provide the intracellular machinery for appropriate post-translational modification of the proteins. Bacterial expression systems are also not the system of choice in many instances because some bacterial products, such as the bacterial lipopolysaccharide (LPS), are toxic to humans.

Mammalian expression cell systems produce appropriately modified  
25 proteins. They are not the systems of choice for producing many proteins, though, because they generally require the use of immortalized cell lines that also include proteins that transform cells, and because they are more expensive to maintain.

Yeast expression systems provide the same ease of cultivation on  
30 inexpensive growth media as do bacteria. They also provide the same ease of

manipulation of heterologous expression vectors. They are advantageous over bacterial expression systems because they allow expression of proteins with appropriate post-translational modifications, such as proteolytic processing, folding, disulfide bridge formation, and glycosylation. Yeasts have also proven to be safe for human consumption through years of use in food and beverage production. Yeasts have also been used for large-scale production of human, animal, viral, and plant proteins since the early 1980s. Several species of yeast have been used to produce these foreign proteins, including *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Pichia pastoris*, *Hansenula polymorpha*, *Kluyveromyces lactis*, and *Yarrowia lipolytica*.

*Saccharomyces cerevisiae*, with its long history of use in the production of bread and alcoholic beverages, is considered a safe organism for human consumption and has been more thoroughly characterized than any other species. It has therefore been the species of choice for many expression systems. A transmembrane receptor, rat somatostatin receptor type 2, as well as a surface protein, Pfs25 of *Plasmodium falciparum*, are examples of a large number of proteins that have been expressed in a *Saccharomyces* expression system.

Both intracellular and extracellular yeast expression systems have been used for heterologous protein production. Intracellular expression is preferred for proteins that are expressed in the cytoplasm, or for secreted proteins with few or no disulfide bonds. Extracellular expression, or secretion of heterologous proteins into the culture medium, provides the advantage of avoiding toxicity caused by accumulated protein and also allows for simple purification procedures. Passage of the heterologous protein through the secretory pathway also allows the heterologous protein to be post-translationally modified.

In yeast and higher eukaryotic cells Sec18p and NSF, respectively, can interact with SNARE proteins to stimulate secretory traffic in the cell. In yeast, Sec18p works in conjunction with Sec17p to promote protein secretion through sequential membrane vesicle fusion, while in mammalian cells the Sec18p counterpart, N-ethylmaleimide-sensitive factor (NSF), works in conjunction with

the Sec17p mammalian counterpart, alpha-SNAP, to accomplish the same result. The secretory pathways of the two systems are remarkably similar, as indicated by the sequence identity between the proteins associated with each system and the fact that the yeast and mammalian proteins are, to a great extent,

5 interchangeable.

Sec18p has 67% sequence identity with squid NSF, and squid NSF has approximately 75% homology with NSF found in Chinese hamster ovary cells (CHO-NSF) and *Drosophila* NSF (d-SNF1). Schweizer, *et al.*, *Science* (1998) 279: 1203. Furthermore, when Sec18p is introduced into mammalian cells, it has  
10 been shown to interact with synaptic SNARE proteins and to synergize with alpha-SNAP to stimulate exocytosis in those cells, demonstrating that the proteins associated with membrane fusion and protein secretion are conserved from yeast to mammals. Steel, G.J., *et al.*, *Biochemistry* (1999) 38(24): 7764.

The yeast Sec17 gene product has been shown to be functionally  
15 equivalent to the alpha-SNAP protein, exhibiting the exact biochemical properties expected for a yeast homolog of the mammalian transport factor. Griff, I.C., *J. Biol. Chem* (1992) 267: 12106. Yeast cytosol can support mammalian endosomal vesicle fusion, demonstrating that there is conservation between yeast and mammalian cells in terms of cytosolic components required  
20 for vesicle fusion. Woodman, P.G., *Yeast* (1996) 12: 1251.

Unfortunately, production of proteins in *S. cerevisiae*, either intracellularly or through the secretory pathway, results in a limited yield. In cytoplasmic expression systems, this problem has been addressed by fusing the target protein to a stable protein such as human superoxide dismutase (SOD) or  
25 human gamma interferon (IFN $\gamma$ ). A ubiquitin fusion expression system has also been used to increase yield and protein stability.

For secreted proteins, yield has been increased by using methylotrophic yeast, such as *Pichia pastoris* or *Hansenula polymorpha*, as host cells. Although these species have been shown to produce increased amounts of some proteins,  
30 particularly human serum albumin (which is secreted at 4 g/l by *P. pastoris*),

protein secretion still does not regularly occur at a level that makes any of the yeast species efficient sources for heterologous protein production. Furthermore, expression in methylotrophic yeast requires the use of methanol, a highly volatile substance, in the culture environment.

5 In some cases, overexpression of certain proteins in conjunction with the target heterologous protein has been effective for increasing target protein secretion. Human leukocyte protease inhibitor, for example, has been shown to be secreted at a three- to four-fold higher rate when ubiquitin was simultaneously overexpressed from a chromosomal UB14 gene under the control of the GAL1  
10 promoter. Nevertheless, those of skill in the art continue to search for host cells, expression vectors, and methods for increasing protein production and secretion in cellular expression systems.

Therefore, there is a continuing need for improved cellular expression systems that produce higher yields of heterologous proteins and can be subjected  
15 to relatively easy production and purification techniques.

### Summary of the Invention

The invention provides a polynucleotide encoding a functional vesicular fusion factor 2 protein (hereinafter the “*VFF2* nucleotide sequence” and “Vff2  
20 protein” or “Vff2p”, respectively), or a structural or functional homolog of Vff2p. A “structural or functional homolog,” as used herein, is a sequence that is conserved between nucleotide or amino acid sequences, or is a protein that has a conserved structure or function in a cell. In one embodiment, the *VFF2* nucleotide sequence is isolated and may also be free of introns. The *VFF2*  
25 nucleotide sequence may be SEQ ID NO:1. The Vff2p sequence may be SEQ ID NO:2. The isolated polynucleotide may be positioned so as to be expressed under the control of a polynucleotide promoter sequence appropriate in a host cell. Also provided are variants of the *VFF2* nucleotide sequence, such as functionally equivalent insertion, deletion and substitution sequences. These  
30 insertions and/or deletions may be made to non-essential regions of the *VFF2*

sequence. The substitutions may be conserved substitutions. The polynucleotide may also contain a sequence encoding a target protein that is operably linked to a second promoter.

Also provided is a polynucleotide expression vector containing SEQ ID

- 5 NO:1 and related elements necessary for cellular expression of the protein encoded by SEQ ID NO:1. For example, a promoter sequence that directs transcription of SEQ ID NO:1 in a host cell can be incorporated into the polynucleotide expression vector.

Also provided is the Vff2 protein. This protein may be SEQ ID NO:2.

- 10 The Vff2 protein can be about 32 kD in size.

- The invention also provides a recombinant host cell that is a cell genetically altered to express the Vff2 protein. The host cell may be a yeast cell. The yeast cell can be a *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Yarrowia lipolytica*, *Pichia pastoris*, *Hansenula polymorpha*, or *Kluyveromyces*  
15 *lactis* cell. Specifically, the invention provides a yeast secretory mutant that has been genetically altered by transformation with the *VFF2* polynucleotide sequence to secrete enhanced amounts of one or more proteins produced by the cell.

- Furthermore, the invention provides a method for increasing protein  
20 production or secretion from a cell. The method involves the steps of introducing the polynucleotide encoding *VFF2* into a host cell and culturing the host cell under conditions effective to allow expression of the encoded *VFF2* polynucleotide sequence.

- The invention also provides a method of selecting for a yeast secretory  
25 mutant cell containing a *VFF2* nucleotide sequence by growing the recombinant cell at a temperature of about 32-37°C. The secretory mutant cell can be sec17-1, sec18-1, bet1-1, sec22-2, us01-1, pex3-1, sed5-1, cdc48-2, sec7-5, or ypt1-3.28. Specifically it can be sec17-1, sec18-1, bet1-1, sec22-2, us01-1, or pex3-1, and in particular sec18-1.

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### Brief Description of the Drawings

Figure 1. This is a schematic of possible vectors that can be made in accordance with the present invention. Figure 1A depicts a single vector containing both *VFF2* and a gene for a target protein “X”. Figure 1B depicts a combination of two vectors where the first vector has the *VFF2* gene, and the second vector has the gene for a target protein “X”.

Figure 2. This is a schematic drawing of how *VFF2* promotes growth of the *sec18-1* strain and how this is tied to increased secretion.

Figure 3. This figure depicts growth curves for various yeast strains. Figure 3A shows growth at 24°C and Figure 3B shows growth at 37°C.

### Detailed Description of the Invention

Cell growth and division is a tightly regulated process. The yeast cell synthesizes, in a concerted fashion, proteins and lipids to allow for an expansion of the cellular perimeter, ultimately resulting in the generation of a daughter cell. The secretion of lipids and proteins is needed to allow for cellular growth, because the plasma membrane needs to increase in surface area. If sufficient nutrients are available, the cell selects a site on its plasma membrane to generate and grow a bud, representing the daughter cell. Vectorial secretion of proteins and lipid membranes ensures further growth of the bud, until the bud has reached the size of the original mother cell, and intracellular organelles have been partitioned. The two cells will separate by septation, and a new cycle of cell growth and division occurs. Cell growth is dependent on the secretion of vesicles and their cargo. For secretion to occur, vesicles have to fuse with organelles and ultimately the plasma membrane. This fusion process requires numerous secretory proteins, such as, but not limited to, Sec17p, Sec18p, SNAREs and other proteins, that confer specificity of fusion and are participants in the fusion mechanism. Cellular growth is commonly rate limited by availability of nutrients, cell cycle checkpoints and secretion. A common aim is to metabolically engineer production strains of yeast to enhance levels of secretion

and protein production. This can be achieved by identifying the rate limiting steps of key metabolic and cellular pathways, and improving these bottlenecks. Unfortunately, it is not clear what limits the rate of secretion, limiting strategic improvement of secretion.

5           The present invention provides a protein, a polynucleotide sequence encoding the protein, and a method of using the protein to increase intracellular production or secretion of a heterologous protein in a cellular expression system, including yeast and higher eukaryotic cell expression systems. In particular, a novel protein, vesicular fusion factor 2 or “Vff2p”, and its corresponding novel  
10       polynucleotide sequence, *VFF2*, have been discovered and isolated. In addition, a method for using *VFF2* and Vff2p to increase intracellular protein or secreted protein in a cellular expression system has been discovered.

          Proteins acting in a biochemical pathway, such as Vff2p, can be identified by means of a genetic suppression screen. Briefly, a genetic suppression screen  
15       identifies mutations for which the phenotype can be overcome by expression of or addition of a target protein. If the target protein is unknown, it can be identified by its presence in those cells in which the known mutation has been suppressed. According to the present invention, an overexpression suppressor screen has been developed and has enabled the discovery of the Vff2 protein as a  
20       suppressor of mutations in, for example, v-SNARE proteins, t-SNARE proteins, Sec18p, Sec17p, and Ypt1p (a small rab-like GTPase required for initial tethering of vesicles). Eakle, K.A., *et al.*, Mol. Cell Biol. (1988) 16 (15): 7499; Griff, I.C., *et al.*, J. Biol. Chem. (1992) 267 (17): 12106; Pryer, N.K., *et al.*, Annu. Rev. Biochem. (1992) 61: 471; Segev, N., *et al.*, Cell (1988) 52 (6): 915.  
25       Overexpression of the Vff2 protein in such secretory mutants has been discovered to result in at least a two-fold increase in the rate of protein secretion and the cellular biomass.

          Three different groups of secretory mutations have been identified: 1) mutations that are strongly suppressed by *VFF2*, 2) mutations that are suppressed  
30       by *VFF2* but not as strongly, and 3) mutations that are not suppressed by *VFF2*.



Examples of mutations that fall into the first group are sec17-1, sec18-1, bet1-1, sec22-2, uso1-1, pex3-1. With the exception of pex3-1, these mutations can generally be described as mutations in proteins, which are involved early in the secretory pathway and/or involved in the required cellular machinery for

5 membrane fusion. These strains would most likely be usable for selection using high temperature.

Examples of mutations that fall into the second group are sed5-1, cdc48-2, sec7-5, ypt1-3. These mutations are also in the early secretory pathway but are less useful in high temperature selection.

10 Examples of mutations that fall into the last group are ufe1-1, tip20-5, sec20-5, sec18-1sec23-1 (double mutant), sec21-4, vps6, vam3. These mutations are not suppressed by *VFF2*. One thing they have in common is that they are all involved in a step of the secretory pathway that is not part of the secretory apparatus. In other words, these mutations are not in the linear secretory  
15 pathway, as are the group 1 and 2 mutations. Instead, they are in branched pathways not directly involved in the secretion process.

A polynucleotide sequence of the present invention is a sequence encoding a functional Vff2 protein. It is well known that one or more nucleotide substitutions can be made to a polynucleotide sequence without affecting  
20 production of a functional protein. For example, the third nucleotide position of a codon at times may be changed without changing the amino acid encoded by that codon. In some cases, the first and second positions may also be changed without effecting a change in the amino acid encoded by the codon. It is also known that additional nucleotides can be added either 5N or 3N, or both, to a  
25 polynucleotide sequence without affecting expression of a functional protein from that polynucleotide. In fact, it is often desirable to place nucleotides encoding transcriptional or translational elements at positions 5N or 3N to a polynucleotide protein-coding region in order to increase or regulate protein expression. It is also desirable to incorporate the protein-coding polynucleotide  
30 sequence into an appropriate plasmid or other expression vector in order to effect

expression of the desired target protein. Therefore, the present invention includes modifications of a polynucleotide sequence of SEQ ID NO:1, wherein that sequence has been modified by any of the changes previously discussed, has been modified internally, or wherein that sequence or modification thereof has been  
5 linked to added 5N or 3N nucleotides without changing the functionality of the protein expressed therefrom.

A protein sequence of the present invention is an amino acid sequence for a native Vff2p or variant thereof. A “variant” of Vff2p is a polypeptide that is not completely identical to native Vff2p. Such a variant Vff2p can be obtained  
10 by altering the amino acid sequence by insertion, deletion or substitution of one or more amino acids. The amino acid sequence of the protein is modified, for example by substitution, to create a polypeptide having substantially the same or improved qualities as compared to the native polypeptide. The substitution may be a conserved substitution. A “conserved substitution” is a substitution of an  
15 amino acid with another amino acid having a similar side chain. A conserved substitution would be a substitution with an amino acid that makes the smallest change possible in the charge of the amino acid or size of the side chain of the amino acid (alternatively, in the size, charge or kind of chemical group within the side chain) such that the overall peptide retains its spacial conformation but has  
20 altered biological activity. For example, common conserved changes might be Asp to Glu, Asn or Gln; His to Lys, Arg or Phe; Asn to Gln, Asp or Glu and Ser to Cys, Thr or Gly. Alanine is commonly used to substitute for other amino acids. For the purpose of the conserved substitution, the 20 essential amino acids can be grouped as follows: alanine, valine, leucine, isoleucine, proline,  
25 phenylalanine, tryptophan and methionine having nonpolar side chains; glycine, serine, threonine, cystine, tyrosine, asparagine and glutamine having uncharged polar side chains; aspartate and glutamate having acidic side chains; and lysine, arginine, and histidine having basic side chains. *See, for example, L. Stryer, Biochemistry* (2d ed.) p. 14-15; Lehninger, *Biochemistry*, p. 73-75.

The amino acid changes are achieved by changing the codons of the corresponding nucleic acid sequence. It is known that such polypeptides can be obtained based on substituting certain amino acids for other amino acids in the polypeptide structure in order to modify or improve secretory activity or cellular growth or division. For example, through substitution of alternative amino acids, small conformational changes may be conferred upon a polypeptide that result in increased activity. Alternatively, amino acid substitutions in certain polypeptides may be used to provide residues that may then be linked to other molecules to provide peptide-molecule conjugates that retain sufficient secretory properties of the starting polypeptide to be useful for other purposes.

One can use the hydropathic index of amino acids in conferring interactive biological function on a polypeptide, wherein it is found that certain amino acids may be substituted for other amino acids having similar hydropathic indices and still retain a similar biological activity. Alternatively, substitution of like amino acids may be made on the basis of hydrophilicity. Accordingly, it is noted that substitutions can be made based on the hydrophilicity assigned to each amino acid.

In using either the hydrophilicity index or hydropathic index, which assigns values to each amino acid, it is preferred to conduct substitutions of amino acids where these values are  $\pm 2$ , with  $\pm 1$  being particularly preferred, and those with in  $\pm 0.5$  being the most preferred substitutions.

A variant of the invention may include amino acid residues not present in the corresponding native Vff2p or deletions relative to the corresponding native Vff2p. A variant may also be a "fragment" as compared to the corresponding native Vff2p, *i.e.*, only a portion of a full-length protein. "Recombinant" is defined as a peptide or nucleic acid produced by the processes of genetic engineering. The terms "protein," "peptide" and "polypeptide" are used interchangeably herein.

According to the present invention, Vff2p of SEQ ID NO:2 is a yeast protein sequence. This protein is useful for increasing cell mass and secretion of

expressed proteins in yeast. Analyses of various databases have indicated that SEQ ID NO:1 and SEQ ID NO:2 are unique sequences in the yeast *S. cerevisiae*. By doing a BLAST analysis, homologous sequences have been identified in *S. pombe*, the nematode *Caenorhabditis elegans*, and the plant *Arabidopsis*. These  
5 homologous regions are simply open reading frames (ORFs) in the sequenced genome of these organisms. These ORFs have not been studied to date. Vff2p had 36% identity (*i.e.*, identical amino acids) and 56% homology (*i.e.*, the amino acids were of the same structure/function group, as described above) with *S. pombe*; had 25% identity and 46% homology with *Arabidopsis*; and 24% identity  
10 and 40% homology with *C. elegans*. It is quite surprising that there would be a high level of identity and homology in such diverse organisms.

As mentioned previously, however, proteins of the cellular secretory pathway are conserved between a number of unlike species. Therefore, according to the invention, a nucleotide sequence of SEQ ID NO:1, is used to  
15 increase secretion in other eukaryotic cell expression systems, as well as used as a probe to identify proteins of the same function in other cell types. The method of the present invention can therefore be utilized in a variety of cell types, including plant and animal cell expression systems, to increase protein production and secretion.

20 In the method of the present invention, the Vff2 protein is used to increase heterologous protein production and secretion in yeast cells. In other types of cells, Vff2p or Vff2 protein homologs can be used to increase production and/or secretion of heterologous proteins.

Vff2p may be introduced into a host cell by transformation of the host  
25 cell with a polynucleotide encoding the Vff2 protein, such as SEQ ID NO:1. Briefly, the polynucleotide can be incorporated into a suitable expression vector using methods known to those of skill in the art. Examples of yeast cloning and expression vectors include, for example, yeast integrative plasmids (YIps), consisting of bacterial plasmids with an added marker for selection in yeast.

These vectors require integration into the yeast genome for stable inheritance, since they contain no yeast origin of replication.

Yeast replicating plasmids (YRps) contain an origin of replication derived from the yeast chromosome. The plasmids can replicate without being integrated  
5 into the chromosome. One should keep in mind, however, that since yeast reproduce by budding, YRps are frequently lost in the offspring and therefore require the use of suitable selection techniques.

Yeast centromeric plasmids (YCps) can be used where a low copy number is desired, such as where a protein will accumulate to toxic levels within  
10 the cell before being secreted. The centromeric sequence incorporated into the YCp allows it to function like a chromosome during cell division. The YCp is therefore distributed to daughter cells of each generation and is more stable without maintenance by selection.

Yeast artificial chromosomes (YACs) provide an advantage, according to  
15 the invention, particularly where *Vff2p* is expressed in conjunction with a target heterologous protein from the same expression vector, because there is relatively no limit to the amount of foreign DNA that can be cloned into a YAC. Since the YAC contains an autonomously replicating sequence, a centromeric sequence, and a telomere at each end, it can be consistently transmitted to daughter cells.

A vector that allows for high-level expression of the *VFF2* polynucleotide  
20 sequence is a yeast expression plasmid (YEp), which contains the origin of the endogenous, autonomously replicating high-copy-number 2micron plasmid. YEPs, though poorly segregated into daughter cells, are stably maintained because of their high copy number. When the entire 2micron plasmid DNA is  
25 inserted into yeast cells lacking an endogenous plasmid, copy numbers in excess of 200 per cell can be achieved.

The *Vff2* protein (SEQ ID NO:2) of the present invention can be expressed from the *VFF2* polynucleotide sequence (SEQ ID NO:1) under the control of any one of a variety of suitable promoters. Many suitable promoters  
30 are described in the prior art. The promoter may be a constitutive promoter, or

may be an inducible promoter. For example, a constitutive promoter may be used when a constant high level of expression is desired. Alternatively, a temperature-sensitive promoter may be used. Regulatable promoters used in yeast expression systems include, for example, the upstream sequence for the alcohol dehydrogenase gene (ADH2) and the triose phosphate dehydrogenase gene, as well as GAL1, GAL7, or GAL10 in conjunction with GAL4, regulated by galactose. Suitable promoters also include the PHO5 acid phosphatase and CUP1, which codes for metallothionine and is induced by  $\text{Cu}^{2+}$  or  $\text{Zn}^{2+}$ . In methylotrophic yeast, such as *Pichia pastoris* and *Hansenula polymorpha*, the AOX1 or related promoters provide tight repression of transcription by glucose and most other carbon sources, and induction to levels of greater than 1000x in cells shifted to methanol as the sole carbon source. An effective promoter in *S. cerevisiae* is the inducible GAL1/10 promoter, which can be induced to direct transcription of the *VFF2* polynucleotide sequence when host cells are streaked onto plates containing YPGal medium.

Transformation of yeast cells with an expression vector containing the *VFF2* polynucleotide sequence can be accomplished by methods known to those of skill in the art. Briefly, yeast cell walls can be removed by enzyme digestion, and the resulting spheroplasts can be incubated with vector DNA in the presence of calcium and polyethyleneglycol. Alternatively, intact yeast cells can be treated with alkali metal ions, such as  $\text{Li}^+$ , and then incubated with the vector DNA in the presence of polyethyleneglycol. A third method for transforming yeast cells is electroporation, a technique that has been described in the literature and is well known to those of skill in the art.

Selection procedures for maintaining foreign genetic elements in yeast are commonly designed to utilize a yeast host strain that is defective in the biosynthesis of one or more amino acids, purines, or pyrimidines, in conjunction with a vector for the foreign DNA that contains a yeast gene for the missing function. Examples of nutritional selection markers in yeast expression systems include the LEU2 gene (which supports leucine biosynthesis), the URA3 gene

(which supports uracil biosynthesis), and the HIS3 gene (which supports histidine biosynthesis). Cells deficient in any of the genes needed for biosynthesis of nutritional molecules cannot be grown on minimal medium. Therefore, cells that have successfully incorporated the marker DNA can be

5 selected on the basis of their ability to survive and grow on minimal media. This is particularly useful to inhibit the proliferation of undesired yeast strains.

In the method of the present invention, the *VFF2* polynucleotide sequence is transferred to a yeast secretory mutant, such as, for example, sec18-1 or sec17-1. Yeast secretory mutants are functionally defective in one or more of the  
10 proteins involved in the yeast secretory pathway. A good secretory mutant for use in the method of the present invention is sec18-1.

A target protein may also be introduced into the host cell, by methods previously described. The target protein can be introduced into the host cell in conjunction with the *VFF2* polynucleotide sequence by, for example,  
15 incorporating the nucleotide sequence encoding the target heterologous protein into the same expression vector into which the nucleotide sequence of the *VFF2* polynucleotide sequence has been incorporated, under the control of a different promoter (Figure 1A). Alternatively, the host cell can be transformed with two vectors, the first containing the polynucleotide encoding the Vff2 protein and the  
20 second containing the polynucleotide sequence encoding the target protein (Figure 1B).

To achieve secretion of the target protein from the yeast host cells in the method of the present invention, a signal recognition sequence, or signal peptide, is incorporated at the 5N end of the target protein sequence in the expression  
25 vector. Suitable signal sequences can be chosen from among a number of sequences known to those of skill in the art and include, for example, the signal sequence from secreted invertase (SUC2), secreted acid phosphatase (PHO5), or yeast mating factor alpha.

When sec18 mutants are shifted from the permissive temperature of 20° C  
30 to the restrictive temperature of about 37° C, the secretory pathway has been

shown to be blocked between the endoplasmic reticulum and Golgi elements, and also at the plasma membrane. (Morin-Ganet, M.N., Anat. Rec. (1998) 251(2): 256-264.) When sec18 mutants are transformed with an expression construct containing the *VFF2* polynucleotide sequence, as in the method of the present invention, however, the blockage in the secretory pathway is not observed. In fact, overexpression of the Vff2 protein in secretory mutants, such as the sec18-1 mutant, gives a higher rate of cellular protein secretion and an increase in cellular biomass (*i.e.*, more cells per volume of media) that is at least about 2x higher than that of wild type strains. Furthermore, not only is the mutant rescued at the restrictive temperature, but also the strain grows several times faster than the wild type strain under the same growth conditions (Figure 2). This control of growth by temperature can also be used according to the invention to select transformed cells without the need to incorporate an additional phenotype solely for the purpose of selection.

15       The present invention also provides a genetically altered cell such as a sec 18-1 mutant altered to express or overexpress the Vff2 protein, with increased capacity for heterologous protein secretion. Schweden, *et al.* (U.S. Patent No. 5,672,487, the disclosure of which is incorporated herein by reference) describe a process for recombinant production of proteins in yeast, using the leader sequence of an animal peptide neurohormone to direct secretion of the recombinant protein. Hitzeman, *et al.* (U.S. Patent No. 4,775,622, the disclosure of which is incorporated herein by reference) also describe the expression, processing and secretion of heterologous protein by yeast. Using leader sequences derived from the secretion signal sequences of mammalian interferon genes, they produced a heterologous protein product that was successfully secreted into the growth medium. Hinnen, *et al.* (U.S. Patent No. 5,436,136, the disclosure of which is incorporated herein by reference) also describe upstream activation sites from the yeast PHO5 gene that provide inducible promoters in yeast expression systems. Techniques for producing heterologous proteins in yeast cell expression systems are therefore known to those of skill in the art, and



a variety of techniques and genetic elements can be successfully employed for heterologous protein expression. The protein, polynucleotide sequence, and method of the present invention provide means for increasing protein production and secretion in any of these systems.

5

#### Increasing Protein Secretion in Large-Scale Fermentation

In batch fermentation processes, the sterile growth medium is inoculated with an appropriate yeast strain and the fermentation is carried out without additional growth medium. In the method of the present invention, the inoculum  
10 is provided as a subculture of yeast cells genetically altered to express the *VFF2* polynucleotide sequence in conjunction with a target heterologous protein. The yeast cells can be, for example, yeast species such as *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Yarrowia lipolytica*, *Pichia pastoris*, *Hansenula polymorpha*, or *Kluyveromyces lactis*. Cells should be chosen from secretory  
15 mutants of the species. A good secretory mutant for use in conjunction with *VFF2* overexpression is the *Saccharomyces cerevisiae* sec18-1 mutant.

Cells are cultured through the stationary growth phase, and then harvested. When a secreted protein is the target protein, the protein can be isolated from the culture medium, as yeast generally secretes few proteins.  
20 Where the target protein is not secreted, a higher internal concentration is expected due to the increased protein production and translation machinery produced as a result of over-expression of *VFF2*.

A particular advantage of the claimed sequence and method of the present invention is the use of a secretory mutant cell over-expressing *VFF2* in  
25 continuous fermentation. The cost of producing a specific amount of biomass is potentially much lower using continuous fermentation rather than batch fermentation. Continuous fermentations can be performed in smaller bioreactors than are batch fermentations, medium can be removed in smaller aliquots over time, making protein purification easier without requiring large-scale purification  
30 equipment and techniques, and continuous fermentations can be performed

without the usual interruptions in fermentation processes that are characteristic of batch fermentations. Briefly, a subculture of yeast cell transformants expressing the *VFF2* polynucleotide sequence is inoculated into a volume of appropriate medium. The yeast cell transformants can be chosen from among a number of yeast species, including, for example, *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Yarrowia lipolytica*, *Pichia pastoris*, *Hansenula polymorpha*, or *Kluyveromyces lactis*. Cells should be chosen from secretory mutants of the species. A good secretory mutant for use in conjunction with *VFF2* over-expression is the *Saccharomyces cerevisiae* sec18-1 mutant.

As the fermentation progresses over time, medium and cells are removed, and fresh medium is introduced into the fermentation vessel. The removed medium and cells can be separated by processes known to those of skill in the art, and the protein isolated from the appropriate fraction. Where the target protein is a secreted protein, the target protein can be isolated from the medium. Where the target protein is not a secreted protein, the target protein can be isolated from the cells, which have an increased intracellular protein concentration due to over-expression of the *VFF2* polynucleotide sequence.

The secretion system can be used for recombinant target proteins that require either O-linked or N-linked glycosylation for biological activity. To facilitate protein secretion, an appropriate polynucleotide coding sequence for a signal peptide is functionally linked to the polynucleotide coding sequence of the target protein. The pre-pro-alpha-factor, or leader peptide coding sequence of the yeast mating type factor alpha1 gene is often cloned upstream of the target protein cDNA in order to route the protein for secretion. As the protein enters the secretory pathway and ultimately is exported from the cell, appropriate post-translational modifications are made, and the leader peptide is removed by an endogenous endoprotease that recognizes the dipeptide sequence Lys-Arg. Positioning the Lys-Arg sequence appropriately immediately upstream from the cDNA sequence insures that, following removal of the leader peptide, the target protein will have the appropriate amino acid residue at its N-terminus.

A number of recombinant target proteins have previously been expressed in *S. cerevisiae*, including the Hepatitis B virus surface antigen, the malaria circumsporozoite protein, the HIV-1 envelope protein, a variety of HIV-1 antigens and Hepatitis C proteins, human insulin, human epidermal growth factor, insulin-like growth factor, platelet-derived growth factor, proinsulin, alpha-1 antitrypsin, factor XIIIa (for blood coagulation), and granulocyte-macrophage colony-stimulating factor.

These and other proteins can be produced at higher levels, and more easily purified, using the method of the present invention, in conjunction with standard cell culture and protein purification methods known to those of skill in the art.

#### Increased Production of Enzymatic Biocatalysts

Biotechnology provides a powerful technology for producing cleaner industrial processes and products. It is well known that enzymes provide valuable catalysts for a growing number of industrial processes. Biocatalytic enzymes provide the catalytic activity while minimizing waste generation and the number of process steps.

A significant example of the use of microorganisms, particularly yeast, as biocatalysts is provided by Gavagan, *et al.* (*J. Org. Chem.* (1997) 62: 549). The process, developed by the DuPont Company, produces glyoxylic acid from glycolic acid using a cellular transformant expressing an enzymatic catalyst derived from spinach and yeast. In U.S. Patent No. 5,834,262 (incorporated herein by reference), Anton *et al.* describe a related process using the enzyme glycolate oxidase in the form of a microbial cell transformant that intracellularly expresses and retains in the cytoplasm or peroxisomes glycolate oxidase selected from the group consisting of transformants of *Aspergillus nidulans*, *Hansenula polymorpha*, *Pichia pastoris*, and *Escherichia coli*, under conditions where the transformants are permeabilized to the passage of carboxylic acids.

The sequence and method of the present invention provide increased secretion of biocatalytic molecules, such as the enzymes glycolate oxidase or catalase, for example.

Fernandez-Lafuente *et al.* (Tetrahedron Letters (1997) 38: 4693)

- 5 described the synthesis of a second-generation cephalosporin, Cefalozin, from cephalosporin C. The method of synthesis involved using three consecutive biotransformations catalyzed by D-aminoacid oxidase, glutaryl acylase and penicillin acylase. Although conventional synthesis involved toxic reagents for chemical activation of the acyl donor carboxylic groups, as well as the use of  
10 chlorinated solvents, the biocatalytic process allowed synthesis in one reaction vessel, did not involve toxic reagents or products, and reduced the steps needed to purify the protein.

#### High-Throughput Screening Using VFF2 Secretion Method

- 15 The sequence and method of the present invention also provide an improved method for high-throughput screening of compounds using yeast expression systems. High-throughput screening methods are known to those of skill in the art, and may rely upon various detection techniques, such as chemiluminescence, fluorescence, morphological, and absorbance assays.
- 20 Chemiluminescent assays often use the bioluminescent substrate for luciferase, luciferin. The calcium ion-sensitive photoprotein aequorin is also used in chemiluminescent assays. Fluorescence assays are divided into at least three major categories: (1) intensity-based assays, in which the prototypic intensity-based indicator is Fluo-3, a fluorescein-based intracellular calcium ion sensor that  
25 increases its fluorescence intensity by about 100x when calcium is bound; (2) fluorescence resonance energy transfer (FRET), which results when two fluorophores (donor and acceptor) come in close proximity (excitation energy is transferred from the donor to the acceptor, decreasing donor intensity and increasing acceptor intensity), and (3) fluorescence localization or redistribution,  
30 which relies on the molecular translocation apparatus associated with cellular

signaling. Examples of FRET probes include CCF2 (a beta-lactamase) and cou-  
lipids and oxonols. The most common probes for fluorescence localization or  
redistribution are chimeric green fluorescent proteins (GFPs).

Yeast-based high-throughput screens take advantage of the fact that  
5 yeasts grow rapidly, are easy and economical to culture, and can be easily  
genetically manipulated. G-protein coupled receptors (GPCRs), for example,  
have been successfully expressed in yeasts, as have proteins such as the human  
beta2-adrenergic receptor (expressed in *S. cerevisiae* under the control of the  
GAL1 promoter), a modified human beta2-adrenergic receptor (expressed in *S.*  
10 *pombe*), a human M1 muscarinic receptor, rat M5 muscarinic acetylcholine  
receptor, and a modified form of the mouse 5HT5a serotonin receptor (all  
expressed in *S. cerevisiae*). The native human dopamine D2s receptor has been  
expressed in both *S. cerevisiae* and *S. pombe*. In addition to the G-protein  
coupled receptors, yeasts have been used to express functional ion channels,  
15 mammalian peptide hormones, extracellular hormone ligand-binding proteins,  
and protein tyrosine kinases.

Given the wide variety of proteins that can be expressed, either as  
intracellular proteins or as secreted proteins, the method of the present invention  
provides an enhancement of high-throughput screening methods, allowing for  
20 greater ease of detection due to increased protein concentrations per well. High-  
throughput screening is performed, for example, in 96-well microtiter plates or in  
microtiter plates containing more than 96 wells. The quantity of cells cultured  
therein is therefore smaller than in larger culture vessels. A significant  
improvement in intracellular protein concentration, or in protein secretion, as  
25 provided by the sequence and method of the present invention, allows detection  
of reactive compounds with a smaller cell culture. Thus the sequence and  
method of the present invention facilitates high-throughput screening by  
increasing the concentration of target proteins in the screening samples.

The *S. cerevisiae* Sec18-1 *VFF2* Strain of the Present Invention Can Be Used in Protein Expression Systems, in Biocatalysis, or in High-Throughput Screening

The sec18-1 *VFF2* *S. cerevisiae* strain of the present invention was  
5 produced by transforming a sec18-1 temperature-sensitive strain with a yeast centromeric plasmid that contains the *VFF2* gene behind the GAL1 promoter. This plasmid also contained the URA3 selectable marker so that transformants could be selected on minimal media lacking uracil.

The resulting cells exhibit greater cellular biomass and increased protein  
10 secretion relative to wild type *S. cerevisiae* strains for a given amount of time. These cells can be transformed with appropriate expression vectors containing any of a number of foreign polynucleotide sequences, such as a target protein that may be toxic internally to a cell, but is not if secreted externally. Such secreted proteins can then be harvested from the media.

15 The cells can also be transformed with appropriate expression vectors containing the polynucleotide sequence of a catalytic enzyme to produce a biocatalyst, secreting the enzyme at a rate higher than that obtained from wild type cells. Furthermore, the cells are ideal for high-throughput screening of a variety of compounds that interact with, for example, G-protein coupled  
20 receptors, hormones, and protein tyrosine kinases.

## EXAMPLES

### Example 1: Genetic screen

The purpose of this genetic screen was to identify potential genes that  
25 genetically interact with or can compensate for the loss of the *SEC17* gene in the budding yeast, *Saccharomyces cerevisiae*. The Sec17 protein is a yeast homolog of the mammalian protein alpha-SNAP that is involved in the process of membrane fusion and secretion in the cell.

A temperature-sensitive (ts) *sec17-1* strain was transformed with an  
30 overexpression *S. cerevisiae* cDNA library. This library consisted of plasmids with a selectable auxotrophy marker and a cDNA fragment behind a galactose-

inducible promoter sequence. The colonies obtained from the transformation were replica plated and placed at 37°C, the non-permissive temperature for the *sec17-1* strain. Colonies that subsequently grew at 37°C were selected and the plasmid they harbored was isolated. This plasmid was re-transformed into the same strain to confirm the suppression of the *sec17-1* temperature sensitive phenotype. The plasmid was then transformed into *E. coli* for plasmid mini-preps. One such plasmid was later identified to contain a novel ORF, which was named *VFF2*.

#### 10 Example 2: Sequence identification

A mini-prep of the plasmid was sent along with standard T3/T7 sequencing primers, was sequenced at the in-house sequencing facility at the Salk Institute.

The sequence was then placed in a search in the Saccharomyces Genome Database and was identified as the ORF YDR361c, consisting of 852 base pairs encoding a protein of 283 amino acids. From the predicted protein structure, the full length protein should be around 32 kDa.

A BLAST search for homologies with other gene sequences entered into the NCBI GenBank did not turn up any significant homology with other known genes. A BLAST search for homologies with other protein sequences turned up *Schizosaccharomyces pombe*, *Arabidopsis thaliana*, and *Caenorhabditis elegans* hypothetical proteins that are 56-40% homologous.

#### Example 3: Characterization of *VFF2*

##### 25 A. Suppression of other secretory mutations by *VFF2*:

The purpose of the present experiment was to determine if the overexpression of *VFF2* could suppress the temperature sensitive phenotype of other secretory (sec) mutant strains.

The original overexpression plasmid isolated from the genetic screen that contained *VFF2* was transformed it into other sec mutants. A control plasmid

was also constructed in which the *VFF2* cDNA was cut out and the vector was closed by religating. This was done to ensure that the suppression phenotype was correlated with the presence of the *VFF2* polynucleotide sequence and not just an effect of the vector or the GAL promoter. Once the sec mutant strains that  
5 contained these plasmids was obtained, the strains were struck on plates containing galactose, allowed to grow at the permissive temperature for 6-12 hours, and then shifted to the non-permissive temperature of 37°C for 48 hours. As a negative control, a strain that has a temperature sensitive mutation in topoisomerase II, a DNA replication enzyme, but should otherwise exhibit  
10 normal secretory processes, was transformed.

Overexpression of *VFF2* can suppress the ts phenotype of a variety of sec mutants including *sec18-1* (the yeast homolog of mammalian NSF, an ATPase involved in membrane fusion), *bet1-1* and *sec22-2* (two t-SNARE molecules involved in ER-to-Golgi fusion, and *cdc48-2* (an ATPase similar to NSF that  
15 participates in ER-ER homotypic fusion). Overexpression of *VFF2* did not suppress the topoisomerase mutation and did not suppress *ufe1-1* (a t-SNARE involved in ER-ER fusion and retrograde or Golgi-to-ER traffic). No effect was seen in any strain containing only the control plasmid.

*VFF2* can suppress a variety of secretory mutations in the ER-to-Golgi  
20 pathway but not in the retrograde, Golgi-to-ER pathway. Furthermore, *VFF2* is a strong suppressor of the *sec18-1* mutation that has never been found to be suppressed by any other polynucleotide sequence before.

## B: Depletion experiments

25 Depletion experiments were performed to determine how much Vff2 protein is needed to rescue a *VFF2* knockout strain.

A *VFF2* heterozygous diploid (*VFF2* is deleted on one copy of the genome) strain was obtained from Research Genetics. A knockout of YDR361c was requested. The deletion of this gene is lethal, which was confirmed by  
30 sporulating the diploid and dissecting tetrads, of which only the two that still had



the intact *VFF2* polynucleotide sequence were viable. The diploid strain was transformed with the above-described *VFF2* overexpression plasmid and sporulated. Tetrads were dissected on plates containing galactose to induce overexpression of the plasmid copy of *VFF2*. Spores were then selected that had  
5 the genomic copy of *VFF2* deleted and harbored the plasmid were selected. The colonies that grew up from these spores were then streaked onto plates containing 2%, 1.5%, 1%, 0.5%, and 0% galactose.

There was no detectable difference in growth between 2% and 0.5% galactose plates and all of the strains tested grew robustly. The strains grew more  
10 weakly on the plates that contained 0% galactose.

Because the GAL promoter that was used is known to be a somewhat “leaky” system, it is likely that even in the absence of galactose, a few copies of *VFF2* are being expressed from the plasmid. Growth on 0% galactose plates is then interpreted to mean that even a few copies of the Vff2 protein are sufficient  
15 to rescue a cell that lacks a genomic copy of *VFF2*.

### C. Cellular localization of Vff2 protein

Experiments were also performed to determine the cellular localization of the Vff2 protein.

20 A green fluorescent protein (GFP)-Vff2 fusion protein was made by placing *VFF2* behind the GFP polynucleotide sequence on a yeast expression vector including a galactose-inducible promoter. This plasmid was transformed into a wild type yeast strain. This strain was then grown in media containing 2% galactose to induce expression of the GFP-Vff2 protein. The live cells were  
25 visualized on a deconvolution microscope.

The fusion protein localized predominantly to the nuclei of the cells. It is unclear whether staining in the cytoplasm is localized to membranous structures or is diffuse throughout the cell.

### 30 D. Growth curves for strains overexpressing *VFF2*

It was observed during the suppression experiments that certain strains overexpressing *VFF2* seemed to grow better on plates than their original parent strain even at permissive temperature. In fact, even the wild type strain overexpressing *VFF2* outgrew the wild type strain without the *VFF2* plasmid.

5 This observation led to the hypothesis that if overexpression of *VFF2* leads to increased cell growth, it must also increase secretion of the plasma membrane and the proteins that make up the cell wall, as this is necessary for growth and division of yeast cells. In order to assess the levels to which growth was increased in these cells, growth curve experiments were performed.

10 Growth curves were generated for four different strains: RSY255 (a wild type strain with a similar genetic background to most of the sec mutants used in the above experiments), RSY255 + *VFF2*, sec18-1, and sec18-1 + *VFF2* (Figure 3A and 3B). Each strain was grown in liquid media containing 2% galactose overnight at the permissive temperature. The next day, each strain was reset to a  
15 density of  $3 \times 10^6$  cells/mL and then every two hours an optical density (O.D.) reading was taken for 22 hours. In another set of experiments, the cultures were shifted to the non-permissive temperature of 37°C after being reset to  $3 \times 10^6$  cells/mL.

For the experiment carried out at 24°C, the RSY255 and sec18-1 strains  
20 grew in a logarithmic fashion and at the end of 22 hours had reached a plateau around  $2.7 \times 10^7$  cells/mL. The RSY255 + *VFF2* and the sec18-1 + *VFF2* strains grew much more rapidly and after only 6 hours were 1.5-fold and 2-fold denser than the RSY255 and sec18-1 cultures, respectively. At the end of 22 hours, the RSY255 + *VFF2* culture had reached a density of  $1.3 \times 10^8$  cells/mL and the  
25 sec18-1 + *VFF2* culture had reached a density of  $2.2 \times 10^8$  cells/mL. This represents a 5-fold difference in growth between the RSY255 strain and the RSY255 + *VFF2* strain and an 8-fold difference in growth between the sec18-1 strain and the sec18-1 + *VFF2* strain.

For the experiment carried out at 37°C, the sec18-1 strain arrested growth  
30 at around  $4.5 \times 10^6$  cells/mL that was expected for this strictly ts strain. RSY255

grew similarly at 37°C and 24°C, giving a logarithmic curve that reached a plateau at 22 hours of  $2.6 \times 10^7$  cells/mL. The RSY255 + *VFF2* and the sec18-1 + *VFF2* strains reached densities of  $1.5$  and  $1.7 \times 10^8$  cells/mL, respectively at 22 hours. This represents a 5.7-fold difference in growth between RSY255 and  
5 RSY255 + *VFF2* and a 38-fold difference in growth between the sec18-1 and the sec18-1 + *VFF2* strains.

The overexpression of *VFF2* is correlated with an increased growth phenotype of both a wild type strain and the sec mutant strain sec18-1. The increased growth is observed at both the 24°C permissive temperature and the  
10 37°C non-permissive temperature. One striking observation is that at both temperatures, the strains overexpressing *VFF2* show no signs of a plateau in their growth curves after 22 hours. In order for these strains to be growing so rapidly, they must be secreting plasma membrane and cell wall components at a higher rate. Any protein that contains a signal peptide that targets it to be secreted  
15 outside of the cell will also be secreted at a higher rate. These proteins are carried inside the membrane vesicle that fuses with the plasma membrane to add more membrane to the growing cell and therefore their secretion is tied to cell growth. By pulse-labeling cells and then precipitating any proteins that have been secreted into the media, a secretion profile of the strains overexpressing  
20 *VFF2* and the original parent strains can be generated.

The invention is described with reference to various specific and preferred embodiments and techniques. It should be understood, however, that many variations and modifications may be made while remaining within the scope of the invention. All referenced publications, patents, and patent documents are  
25 intended to be incorporated by reference, as though individually incorporated by reference.

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15

What is claimed is:

1. A polynucleotide comprising a sequence encoding a functional vesicular fusion factor 2 protein (Vff2p), or a structural or functional homolog of Vff2p.
2. The polynucleotide of claim 1, wherein the Vff2p is a yeast protein involved in the secretory pathway and/or involved in the required cellular machinery for membrane fusion.
3. The polynucleotide of claim 1, wherein the Vff2p comprises SEQ ID NO:2.
4. The polynucleotide of claim 1, comprising SEQ ID NO:1.
5. The polynucleotide of claim 1, wherein the protein is about 32 kD.
6. The polynucleotide of claim 1, further comprising a first promoter operatively linked to the sequence encoding the Vff2p.
7. The polynucleotide of claim 6 wherein the first promoter is a promoter that functions in a host cell to direct transcription of the sequence encoding the Vff2p.
8. The polynucleotide of claim 1, further comprising a sequence encoding a target protein.
9. The polynucleotide of claim 8, further comprising a sequence encoding the target protein operably linked to a second promoter.

10. The polynucleotide of claim 9, wherein the second promoter is a promoter that functions in the host cell to direct transcription of the target protein.
11. The polynucleotide of claim 7, wherein the host cell is a yeast cell.
12. The polynucleotide of claim 2, wherein the yeast is a *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Yarrowia lipolytica*, *Pichia pastoris*, *Hansenula polymorpha*, or *Kluyveromyces lactis*.
13. A polynucleotide expression vector comprising a polynucleotide encoding a functional Vff2p, or a structural or functional homolog of Vff2p.
14. The expression vector of claim 13, where in the Vff2p comprises SEQ ID NO:2.
15. The expression vector of claim 13, comprising SEQ ID NO:1.
16. The expression vector of claim 13, wherein the protein is about 32 kD.
17. The expression vector of claim 13, further comprising a first promoter sequence operatively linked to the sequence encoding the Vff2p.
18. The expression vector of claim 17 wherein the first promoter is a promoter that functions in a host cell to direct transcription of the sequence encoding the Vff2p.
19. The expression vector of claim 13, further comprising a sequence encoding a target protein.

20. The expression vector of claim 19, wherein transcription of the target protein is directed by a second promoter.

21. The expression vector of claim 20, wherein the second promoter is a promoter that functions in the host cell to direct transcription of the target protein.

22. The expression vector of claim 18, wherein the host cell is a yeast cell.

23. The expression vector of claim 22, wherein the protein is from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Yarrowia lipolytica*, *Pichia pastoris*, *Hansenula polymorpha*, or *Kluyveromyces lactis*.

24. A recombinant host cell comprising a cell genetically altered to express a protein encoded by a polynucleotide sequence encoding a functional Vff2p, or a structural or functional homolog of Vff2p.

25. The host cell of claim 24, where in the Vff2p comprises SEQ ID NO:2.

26. The host cell of claim 24, comprising SEQ ID NO:1.

27. The host cell of claim 25, further comprising a sequence encoding a target protein.

28. The host cell of claim 24, wherein the host cell is a yeast cell.

29. The host cell of claim 28, wherein the yeast cell is a *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Yarrowia lipolytica*, *Pichia pastoris*, *Hansenula polymorpha*, or *Kluyveromyces lactis* cell.

30. The host cell of claim 28, wherein the host cell lacks a functional protein involved in the secretory pathway and/or involved in the required cellular machinery for membrane fusion, other than Vff2p.

31. A method for increasing protein production in a cell, comprising introducing Vff2p to a host cell.

32. The method for increasing protein production in a cell according to claim 31, wherein a polynucleotide encoding Vff2p is introduced into the host cell and thereafter, culturing the host cell under conditions effective to allow expression of the encoded Vff2p.

33. A method for increasing protein secretion from a cell, comprising introducing Vff2p to a host cell.

34. The method for increasing protein secretion from a cell according to claim 33, wherein a polynucleotide encoding Vff2p is introduced into the host cell and thereafter, culturing the host cell under conditions effective to allow expression of the encoded Vff2p.

35. An isolated functional vesicular fusion factor 2 protein.

36. The protein of claim 35 having an amino acid sequence essentially corresponding to SEQ ID NO:2.

37. A method of selecting for a yeast secretory mutant cell containing a polynucleotide sequence encoding a Vff2p, or a structural or functional homolog of Vff2p, operably linked to a first promoter, the method comprising growing the recombinant cell at a temperature of about 32-37°C.



38. The method of claim 37, wherein the temperature is at about 37°C.
39. The method of claim 37, wherein the secretory mutant cell is sec17-1, sec18-1, bet1-1, sec22-2, uso1-1, pex3-1, sed5-1, cdc48-2, sec7-5, or ypt1-3.28.
40. The method of claim 39, wherein the secretory mutant cell is sec17-1, sec18-1, bet1-1, sec22-2, uso1-1, or pex3-1.
41. The method of claim 40, wherein the secretory mutant cell is sec18-1.
42. The method of claim 37, wherein the polynucleotide further comprises a sequence encoding a target protein operably linked to a second promoter.

# Sequence and Method for Increasing Protein Expression in Cellular Expression Systems

## Abstract

The invention provides a novel protein that, when expressed in a host cell, increases cellular biomass and cellular protein production and secretion. The invention also provides a polynucleotide encoding the novel protein, and

5 methods for using the polynucleotide and encoded protein to increase cellular biomass and cellular protein production and secretion. Also provided is a genetically altered mutant cell strain with enhanced production and secretion of cellular and heterologous proteins.

"Express Mail" mailing label number: EL505994302US

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A

|  |          |                   |           |          |      |     |                  |     |     |
|--|----------|-------------------|-----------|----------|------|-----|------------------|-----|-----|
|  | GAL 1/10 | Signal<br>peptide | Protein X | GAL 1/10 | VVF2 | ars | amp <sup>r</sup> | neo | ars |
|--|----------|-------------------|-----------|----------|------|-----|------------------|-----|-----|

B

|  |          |      |                  |  |     |     |     |
|--|----------|------|------------------|--|-----|-----|-----|
|  | GAL 1/10 | VVF2 | amp <sup>r</sup> |  | neo | ars | ori |
|--|----------|------|------------------|--|-----|-----|-----|

|  |          |                |           |                  |     |     |     |
|--|----------|----------------|-----------|------------------|-----|-----|-----|
|  | GAL 1/10 | Signal peptide | Protein X | amp <sup>r</sup> | zeo | ars | ori |
|--|----------|----------------|-----------|------------------|-----|-----|-----|

GAL 1/10 = Galactose inducible promoter      vvf2 = vesicular fusion factor 2 gene  
 ori = Origin of replication      zeo = zeocin resistance gene  
 neo = Neomycin resistance      Protein "X" = Protein to be expressed  
 ars = autonomous replicating sequence  
 ampr = Ampicillin resistance

Figure 1

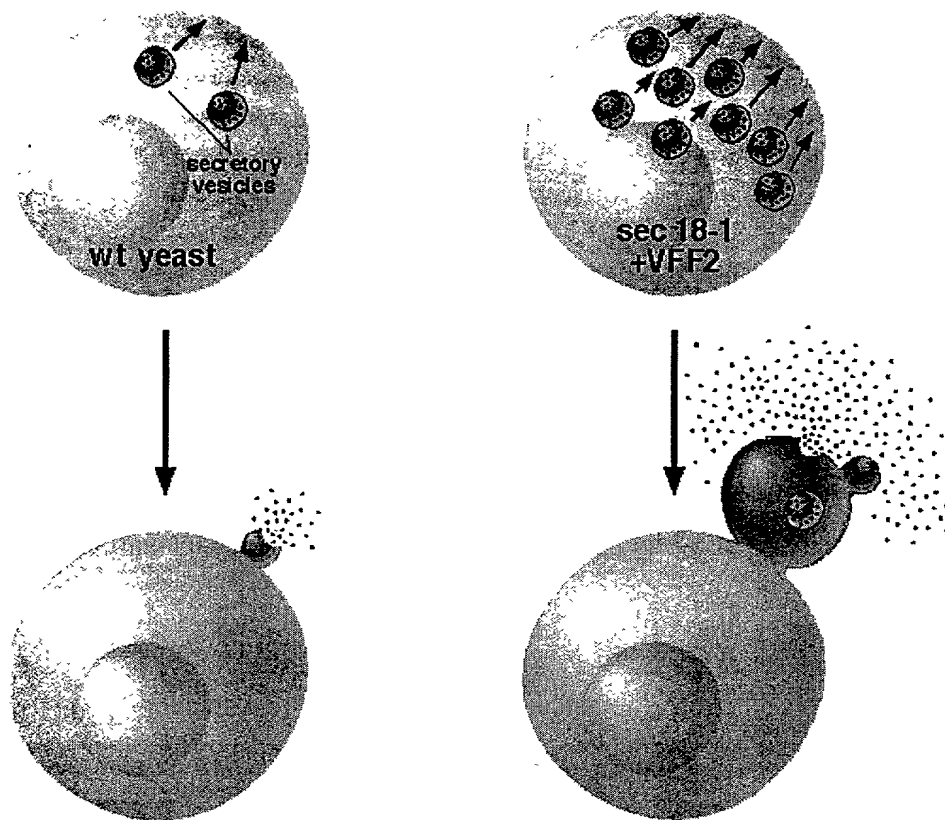
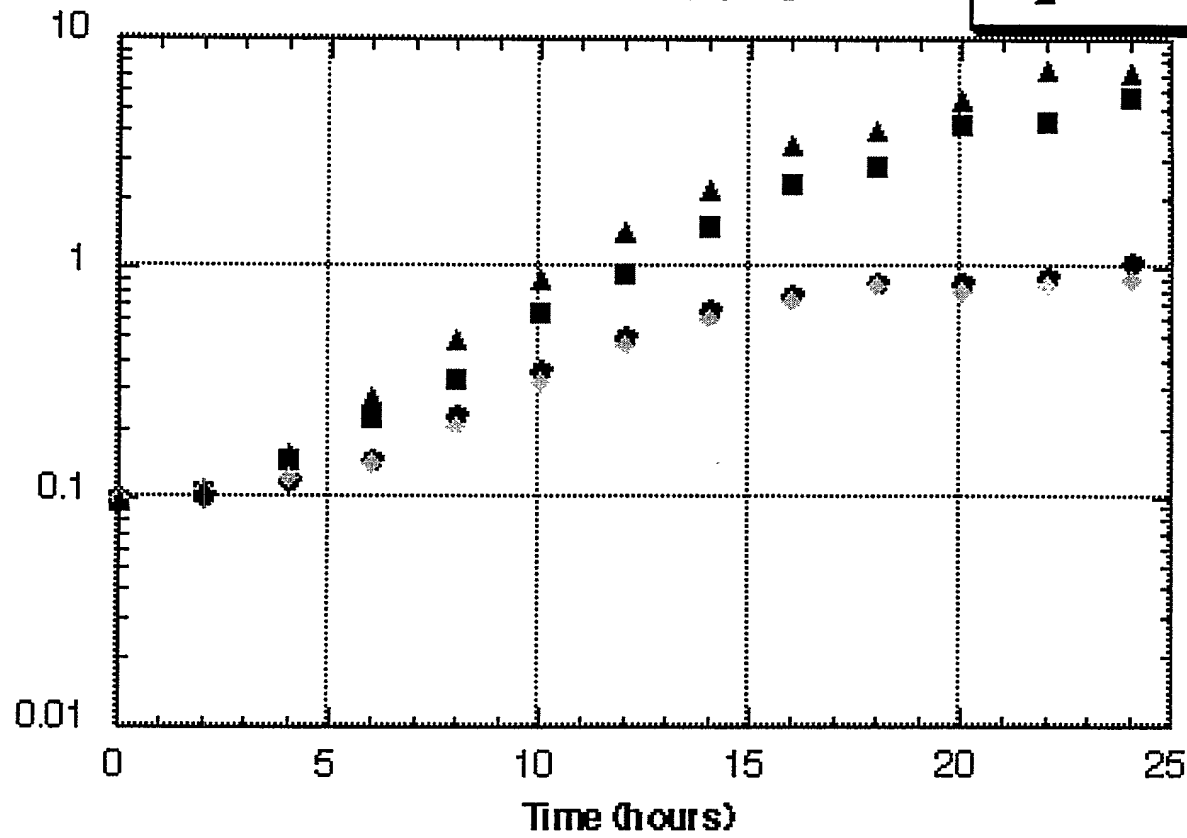


Figure 2

Figure 3A

Growth at 24 °C

Absorbance at 600nm  
(log scale)

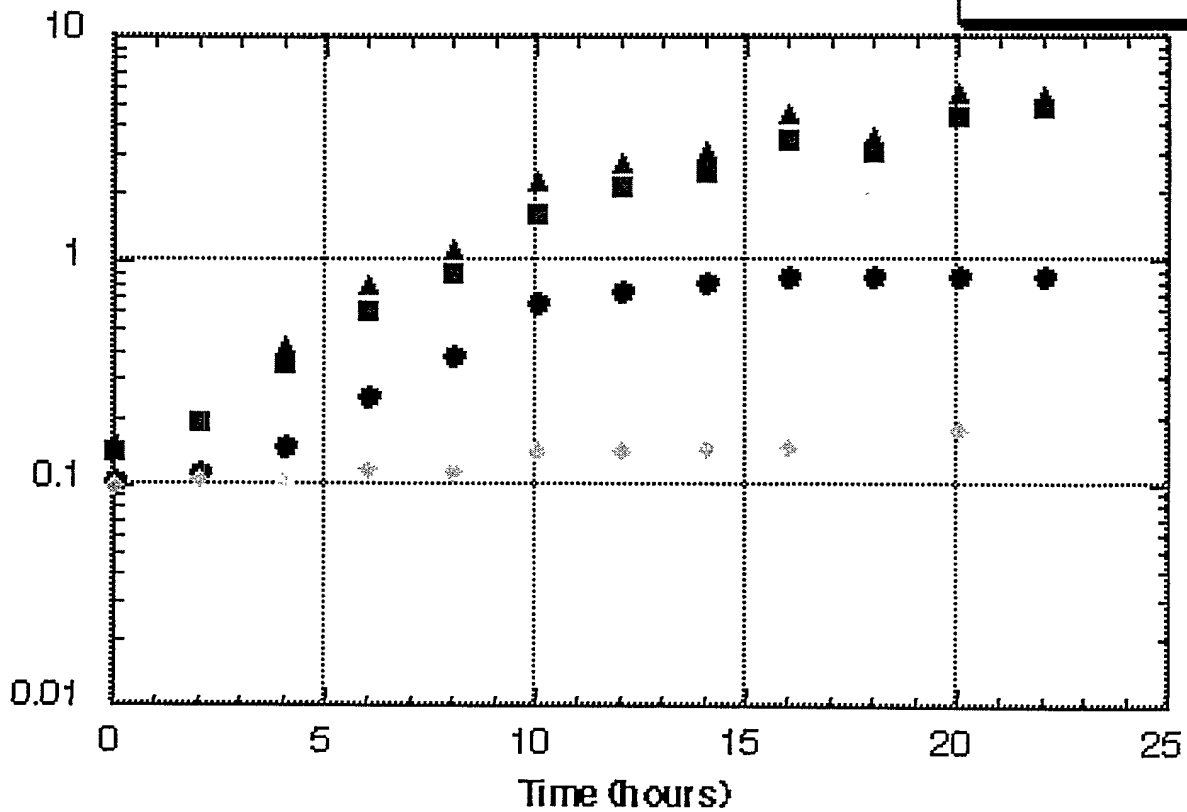


- 255
- 255+VFF2
- sec18-1
- ▲ sec18-1+VFF2

Figure 3B

Growth at 37 °C

Absorbance at 600nm  
(log scale)



- 255
- 255+VFF2
- sec18-1
- ▲ sec18-1+VFF2

**S/N Unknown**

**PATENT**

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

|             |  |                 |             |
|-------------|--|-----------------|-------------|
| Applicant:  | Martin Latterich et al.  | Examiner:       | Unknown     |
| Serial No.: | Unknown  | Group Art Unit: | Unknown     |
| Filed:      | Herewith   | Docket:         | 1211.001US1 |
| Title:      | SEQUENCE AND METHOD FOR INCREASING PROTEIN EXPRESSION IN CELLULAR EXPRESSION SYSTEMS |                 |             |

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**COMMUNICATION UNDER 37 C.F.R. § 1.821**

Assistant Commissioner for Patents  
Washington, D.C. 20231

Sir:

A SEQUENCE LISTING, to conform the above-referenced application to the requirements of 37 C.F.R. §§ 1.821 through 1.825, is submitted herewith.


In accordance with 37 C.F.R. § 1.821(e), a copy of the above-submitted SEQUENCE LISTING in ASCII computer readable form is also submitted herewith. It is respectfully submitted that the contents of the paper version of the SEQUENCE LISTING and the computer readable form being submitted herewith are the same.

Respectfully submitted,

MARTIN LATTERICH ET AL.

By their Representatives,

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# SEQUENCE LISTING

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<120> sequence and method for increasing protein expression in cellular expression systems

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<213> *Saccharomyces cerevisiae*

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| gaaaatggca gtgacgagtc tgaaattgac attagtagca ccgattcaga aaatgaagaa   | 120 |
| gagcaaaatg gagaagaaga gatcgtaaatt attgacttcg attttttcgg tggtaaccca  | 180 |
| gaagttgatt ttcatgcttt aaagaattta ctgcgtcagt tatttggtcc tcaagaaagt   | 240 |
| accaggattc aactaagcag cttggcagat ttgatcctag gttccccaac caccacaatt   | 300 |
| aaaacagacg gcaaagaatc tgatccatac tgttttcttt cattcggtga tttcaaagct   | 360 |
| aatcatctaa gtgattatgt caaatattta caaaaagtgg acatgagact ttccactttc   | 420 |
| ttcaaaaacta tgattgatag tggttaataaa aattgtgctt tggttctcag tgaaaggctg | 480 |
| attaatatgc caccggaagt cgttccacct ttatacaaga ttacgttga ggatgttgcc    | 540 |
| acggcacttg gcgatgacaa acattatgac ttctatatca tcgtcaccag gaagtatgaa   | 600 |
| gtaaattttg aactgacga tgataccgac tctggtaaga ggaataaaaa caaagacgaa    | 660 |
| agatccaaaa aaagggtgaa ggccgatgaa gtagactact ttcatgagga ggaccgattt   | 720 |
| tttgaaaaat atgccaagat tcacttcgaa tcagaagcta aaaagggtgt tatcagctca   | 780 |
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| tccacttggt aa   | 852 |

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Ser Thr Asp Ser Glu Asn Glu Glu Glu Gln Asn Gly Glu Glu Ile
      35             40             45
Val Asn Ile Asp Phe Asp Phe Phe Gly Gly Asn Pro Glu Val Asp Phe
      50             55             60
His Ala Leu Lys Asn Leu Leu Arg Gln Leu Phe Gly Pro Gln Glu Ser
      65             70             75             80
Thr Arg Ile Gln Leu Ser Ser Leu Ala Asp Leu Ile Leu Gly Ser Pro
      85             90             95
Thr Thr Thr Ile Lys Thr Asp Gly Lys Glu Ser Asp Pro Tyr Cys Phe
      100            105            110
Leu Ser Phe Val Asp Phe Lys Ala Asn His Leu Ser Asp Tyr Val Lys
      115            120            125
Tyr Leu Gln Lys Val Asp Met Arg Leu Ser Thr Phe Phe Lys Thr Met
      130            135            140
Ile Asp Ser Gly Asn Lys Asn Cys Ala Leu Val Leu Ser Glu Arg Leu
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Ile Asn Met Pro Pro Glu Val Val Pro Pro Leu Tyr Lys Ile Thr Leu
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Glu Asp Val Ala Thr Ala Leu Gly Asp Asp Lys His Tyr Asp Phe Tyr
      180            185            190
Ile Ile Val Thr Arg Lys Tyr Glu Val Asn Phe Asp Thr Asp Asp Asp
      195            200            205
Thr Asp Ser Gly Lys Arg Asn Lys Asn Lys Asp Glu Arg Ser Lys Lys
      210            215            220
Arg Val Lys Ala Asp Glu Val Asp Tyr Phe His Glu Glu Asp Arg Phe
      225            230            235            240

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Glu | Lys | Tyr | Ala | Lys | Ile | His | Phe | Glu | Ser | Glu | Ala | Lys | Lys | Gly |
|     |     |     |     |     | 245 |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Ile | Ser | Ser | Tyr | Met | Ile | Leu | Asp | His | Glu | Gly | Leu | Val | Lys | Ser |
|     |     |     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |
| Ile | Asp | Glu | Leu | Glu | Thr | Glu | Ile | Ser | Thr | Trp |     |     |     |     |     |
|     |     |     |     |     | 275 |     |     |     | 280 |     |     |     |     |     |     |

SCHWEGMAN, LUNDBERG, WOESSNER & KLUTH, P.A.

# United States Patent Application

## COMBINED DECLARATION AND POWER OF ATTORNEY

As a below named inventor I hereby declare that: my residence, post office address and citizenship are as stated below next to my name; that

I verily believe I am the original, first and joint inventor of the subject matter which is claimed and for which a patent is sought on the invention entitled: **SEQUENCE AND METHOD FOR INCREASING PROTEIN EXPRESSION IN CELLULAR EXPRESSION SYSTEMS.**

The specification of which is attached hereto.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to the patentability of this application in accordance with 37 C.F.R. § 1.56 (attached hereto). I also acknowledge my duty to disclose all information known to be material to patentability which became available between a filing date of a prior application and the national or PCT international filing date in the event this is a Continuation-In-Part application in accordance with 37 C.F.R. § 1.63(e).

I hereby claim foreign priority benefits under 35 U.S.C. § 119(a)-(d) or 365(b) of any foreign application(s) for patent or inventor's certificate, or 365(a) of any PCT international application which designated at least one country other than the United States of America, listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on the basis of which priority is claimed:

**No such claim for priority is being made at this time.**

I hereby claim the benefit under 35 U.S.C. § 119(e) of any United States provisional application(s) listed below:

**No such claim for priority is being made at this time.**

I hereby claim the benefit under 35 U.S.C. § 120 or 365(c) of any United States and PCT international application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT international application in the manner provided by the first paragraph of 35 U.S.C. § 112, I acknowledge the duty to disclose material information as defined in 37 C.F.R. § 1.56(a) which became available between the filing date of the prior application and the national or PCT international filing date of this application:

**No such claim for priority is being made at this time.**

I hereby appoint the following attorney(s) and/or patent agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith:

|                        |                 |                             |                 |                       |                   |
|------------------------|-----------------|-----------------------------|-----------------|-----------------------|-------------------|
| Adams, Gregory J.      | Reg. No. 44,494 | Huebsch, Joseph C.          | Reg. No. 42,673 | Nelson, Albin J.      | Reg. No. 28,650   |
| Anglin, J. Michael     | Reg. No. 24,916 | Jurkovich, Patti J.         | Reg. No. 44,813 | Nielsen, Walter W.    | Reg. No. 25,539   |
| Bianchi, Timothy E.    | Reg. No. 39,610 | Kalis, Janal M.             | Reg. No. 37,650 | Oh, Allen J.          | Reg. No. 42,047   |
| Billion, Richard E.    | Reg. No. 32,836 | Kaufmann, John D.           | Reg. No. 24,017 | Padys, Danny J.       | Reg. No. 35,635   |
| Black, David W.        | Reg. No. 42,331 | Klima-Silberg, Catherine I. | Reg. No. 40,052 | Parker, J. Kevin      | Reg. No. 33,024   |
| Brennan, Leoniede M.   | Reg. No. 35,832 | Kluth, Daniel J.            | Reg. No. 32,146 | Peacock, Gregg A.     | Reg. No. 45,001   |
| Brennan, Thomas F.     | Reg. No. 35,075 | Lacy, Rodney L.             | Reg. No. 41,136 | Perdok, Monique M.    | Reg. No. 42,989   |
| Brooks, Edward J., III | Reg. No. 40,925 | Leffert, Thomas W.          | Reg. No. 40,697 | Polglaze, Daniel J.   | Reg. No. 39,801   |
| Chu, Dinh C.P.         | Reg. No. 41,676 | Lemaire, Charles A.         | Reg. No. 36,198 | Prout, William F.     | Reg. No. 33,995   |
| Clark, Barbara J.      | Reg. No. 38,107 | Litman, Mark A.             | Reg. No. 26,390 | Schumm, Sherry W.     | Reg. No. 39,422   |
| Dahl, John M.          | Reg. No. 44,639 | Lundberg, Steven W.         | Reg. No. 30,568 | Schwegman, Micheal L. | Reg. No. 25,816   |
| Drake, Eduardo E.      | Reg. No. 40,594 | Mack, Lisa K.               | Reg. No. 42,825 | Sliker, Russell D.    | Reg. No. 39,838   |
| Eliseeva, Maria M.     | Reg. No. 43,328 | Maki, Peter C.              | Reg. No. 42,832 | Smith, Michael G.     | Reg. No. P-45,368 |
| Embreton, Janet E.     | Reg. No. 39,665 | Malen, Peter L.             | Reg. No. 44,894 | Steffey, Charles E.   | Reg. No. 25,179   |
| Fogg, David N.         | Reg. No. 35,138 | Mates, Robert E.            | Reg. No. 35,271 | Terry, Kathleen R.    | Reg. No. 31,884   |
| Fordebacher, Paul J.   | Reg. No. 42,546 | McCrackin, Ann M.           | Reg. No. 42,858 | Viksnins, Ann S.      | Reg. No. 37,748   |
| Forrest, Bradley A.    | Reg. No. 30,837 | Nama, Kash                  | Reg. No. 44,255 | Woessner, Warren D.   | Reg. No. 30,440   |
| Harris, Robert J.      | Reg. No. 37,346 |                             |                 |                       |                   |

I hereby authorize them to act and rely on instructions from and communicate directly with the person/assignee/attorney/firm/organization/who/which first sends/sent this case to them and by whom/which I hereby declare that I have consented after full disclosure to be represented unless/until I instruct Schwegman, Lundberg, Woessner & Kluth, P.A. to the contrary.

Please direct all correspondence in this case to **Schwegman, Lundberg, Woessner & Kluth, P.A.** at the address indicated below:  
**P.O. Box 2938, Minneapolis, MN 55402**  
**Telephone No. (612)373-6900**

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Full Name of joint inventor number 1 : **Martin Latterich**  
Citizenship: **United States of America** Residence: **Lo Jolla, California**  
Post Office Address:

Signature: \_\_\_\_\_ Date: \_\_\_\_\_  
Martin Latterich

Full Name of joint inventor number 2 : **Kendall Powell**  
Citizenship: **United States of America** Residence: **Lo Jolla, California**  
Post Office Address:

Signature: \_\_\_\_\_ Date: \_\_\_\_\_  
Kendall Powell

§ 1.56 Duty to disclose information material to patentability.

(a) A patent by its very nature is affected with a public interest. The public interest is best served, and the most effective patent examination occurs when, at the time an application is being examined, the Office is aware of and evaluates the teachings of all information material to patentability. Each individual associated with the filing and prosecution of a patent application has a duty of candor and good faith in dealing with the Office, which includes a duty to disclose to the Office all information known to that individual to be material to patentability as defined in this section. The duty to disclose information exists with respect to each pending claim until the claim is canceled or withdrawn from consideration, or the application becomes abandoned. Information material to the patentability of a claim that is canceled or withdrawn from consideration need not be submitted if the information is not material to the patentability of any claim remaining under consideration in the application. There is no duty to submit information which is not material to the patentability of any existing claim. The duty to disclose all information known to be material to patentability is deemed to be satisfied if all information known to be material to patentability of any claim issued in a patent was cited by the Office or submitted to the Office in the manner prescribed by §§ 1.97(b)-(d) and 1.98. However, no patent will be granted on an application in connection with which fraud on the Office was practiced or attempted or the duty of disclosure was violated through bad faith or intentional misconduct. The Office encourages applicants to carefully examine:

- (1) prior art cited in search reports of a foreign patent office in a counterpart application, and
- (2) the closest information over which individuals associated with the filing or prosecution of a patent application believe any pending claim patentably defines, to make sure that any material information contained therein is disclosed to the Office.

(b) Under this section, information is material to patentability when it is not cumulative to information already of record or being made of record in the application, and

- (1) It establishes, by itself or in combination with other information, a prima facie case of unpatentability of a claim; or
- (2) It refutes, or is inconsistent with, a position the applicant takes in:
  - (i) Opposing an argument of unpatentability relied on by the Office, or
  - (ii) Asserting an argument of patentability.

A prima facie case of unpatentability is established when the information compels a conclusion that a claim is unpatentable under the preponderance of evidence, burden-of-proof standard, giving each term in the claim its broadest reasonable construction consistent with the specification, and before any consideration is given to evidence which may be submitted in an attempt to establish a contrary conclusion of patentability.

(c) Individuals associated with the filing or prosecution of a patent application within the meaning of this section are:

- (1) Each inventor named in the application;
- (2) Each attorney or agent who prepares or prosecutes the application; and
- (3) Every other person who is substantively involved in the preparation or prosecution of the application and who is associated with the inventor, with the assignee or with anyone to whom there is an obligation to assign the application.

(d) Individuals other than the attorney, agent or inventor may comply with this section by disclosing information to the attorney, agent, or inventor.